ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION

Related Applications

This application is a continuation in part of U.S. Application Serial No. 10/251,085 filed September 19, 2002 which claims priority to U.S. Provisional Application No. 60/323,455 filed September 19, 2001.

Technical Field

This disclosure relates to engineered templates useful for amplification of a target nucleic acid sequence. More specifically, templates which are engineered to contain complementary sequences at opposite ends thereof are provided by a nested oligonucleotide extension reaction (NOER). The engineered template allows Single Primer Amplification (SPA) to amplify a target sequence within the engineered template. In particularly useful embodiments, the target sequences from the engineered templates are cloned into expression vehicles to provide a library of polypeptides or proteins, such as, for example, an antibody library.

Background of Related Art

Methods for nucleic acid amplification and detection of amplification products assist in the detection, identification, quantification and sequence analysis of nucleic acid sequences. Nucleic acid amplification is an important step in the construction of libraries from related genes such as, for example antibodies. These libraries can be screened for antibodies having specific, desirable activities. Nucleic acid analysis is important for

detection and identification of pathogens, detection of gene alteration leading to defined phenotypes, diagnosis of genetic diseases or the susceptibility to a disease, assessment of gene expression in development, disease and in response to defined stimuli, as well as the various genome projects. Other applications of nucleic acid amplification method include the detection of rare cells, detection of pathogens, and the detection of altered gene expression in malignancy, and the like. Nucleic acid amplification is also useful for qualitative analysis (such as, for example, the detection of the presence of defined nucleic acid sequences) and quantification of defined gene sequences (useful, for example, in assessment of the amount of pathogenic sequences as well as the determination of gene multiplication or deletion, and cell transformation from normal to malignant cell type, etc.). The detection of sequence alterations in a nucleic acid sequence is important for the detection of mutant genotypes, as relevant for genetic analysis, the detection of mutations leading to drug resistance, pharmacogenomics, etc.

There are many variations of nucleic acid amplification, for example, exponential amplification, linked linear amplification, ligation-based amplification, and transcription-based amplification. One example of exponential nucleic acid amplification method is polymerase chain reaction (PCR) which has been disclosed in numerous publications. See, for example, Mullis et al. Cold Spring Harbor Symp. Quant. Biol. 51:263-273 (1986); Mullis K. EP 201,184; Mullis et al. U.S. Pat. No. 4,582,788; Erlich et al. EP 50,424, EP 84,796, EP 258,017, EP 237,362; and Saiki R. et al. U.S. Pat. No. 4,683,194. In fact, the polymerase chain reaction (PCR) is the most commonly used target amplification method. PCR is based on multiple cycles of denaturation, hybridization of two different oligonucleotide primers, each to opposite strand of the target strands, and

primer extension by a nucleotide polymerase to produce multiple double stranded copies of the target sequence.

Amplification methods that employ a single primer, have also been disclosed. See, for example, U.S. Pat. Nos. 5,508,178; 5,595,891; 5,683,879; 5,130,238; and 5,679,512. The primer can be a DNA/RNA chimeric primer, as disclosed in U.S. Pat. No. 5,744,308.

Some amplification methods use template switching oligonucleotides (TSOs) and blocking oligonucleotides. For example, a template switch amplification in which chimeric DNA primer are utilized is disclosed in U.S. Pat. Nos. 5,679,512; 5,962,272; 6,251,639 and by Patel et al. Proc. Natl. Acad. Sci. U.S.A. 93:2969-2974 (1996).

However the previously described target amplification methods have several drawbacks. For example, the transcription base amplification methods, such as Nucleic Acid Sequence Based Amplification (NASBA) and transcription mediated amplification (TMA), are limited by the need for incorporation of the polymerase promoter sequence into the amplification product by a primer, a process prone to result in non-specific amplification. Another example of a drawback of the current amplification methods is the requirement of two binding events which may have optimal binding at different temperatures as well as the use of primers containing naturally occurring sequences. This combination of factors results in increased likelihood of mis-priming and resultant amplification of sequences other than the target sequence.

Therefore, there is a need for improved nucleic acid amplification methods that overcome these drawbacks. The invention provided herein fulfills this need and provides additional benefits.

Summary

Novel methods of amplifying nucleic acid have now been discovered which include the steps of: a) annealing a primer to a template nucleic acid sequence, the primer having a first portion which anneals to the template and a second portion of predetermined sequence; b) synthesizing a polynucleotide that anneals to and is complementary to the portion of the template between the location at which the first portion of the primer anneals to the template and the end of the template, the polynucleotide having a first end and a second end, wherein the first end incorporates the primer; c) separating the polynucleotide synthesized in step (b) from the template; d) annealing a nested oligonucleotide to the second end of the polynucleotide synthesized in step (b), the nested oligonucleotide having a first portion that anneals to the second end of the polynucleotide and a second portion having the same predetermined sequence as the second portion of the primer; e) extending the polynucleotide synthesized in step (b) to provide a terminal portion thereof that is complementary to the predetermined sequence; and f) amplifying the extended polynucleotide using a single primer having the predetermined sequence.

In an alternative embodiment, the method includes the steps of a) annealing a primer and a boundary oligonucleotide to a template nucleic acid sequence, the primer having a first portion which anneals to the template and a second portion of predetermined sequence; b) synthesizing a polynucleotide that anneals to and is complementary to the portion of the template between the location at which the first portion of the primer anneals to the template and the portion of the template to which the boundary oligonucleotide anneals, the polynucleotide having a first end and a second end,

wherein the first end incorporates the primer; c) separating the polynucleotide synthesized in step (b) from the template; d) annealing a nested oligonucleotide to the second end of the polynucleotide synthesized in step (b), the nested oligonucleotide having a first portion that anneals to the second end of the polynucleotide and a second portion having the same predetermined sequence as the second portion of the primer; e) extending the polynucleotide synthesized in step (b) to provide a terminal portion thereof that is complementary to the predetermined sequence; and f) amplifying the extended polynucleotide using a single primer having the predetermined sequence.

It is also contemplated that a engineered nucleic acid strand having a predetermined sequence at a first end thereof and a sequence complementary to the predetermined sequence at the other end thereof is itself a novel aspect of this disclosure.

In another aspect, this disclosure provides a new method of amplifying a nucleic acid strand that includes the steps of providing an engineered nucleic acid strand having a predetermined sequence at a first end thereof and a sequence complementary to the predetermined sequence at the other end thereof; and contacting the engineered nucleic acid strand with a primer having the predetermined sequence in the presence of a polymerase and nucleotides under conditions suitable for polymerization of the nucleotides.

The amplification processes and engineered templates described herein can be used to prepare amplified products that can be ligated into a suitable expression vector. The vector may then be used to transform an appropriate host organism using standard methods to produce the polypeptide or protein encoded by the target sequence. In particularly useful embodiments, the techniques described herein are used to amplify a

family of related sequences to build a complex library, such as, for example an antibody library.

Brief Description of Drawings

Fig. 1 is a schematic illustration of a primer and boundary oligo annealed to a template;

Fig. 2A is a schematic illustration of a restriction oligo annealed to a nucleic acid strand;

Fig. 2B is a schematic illustration of a primer annealed to a template that has a shortened 5' end;

Fig. 3 is a schematic illustration of an alternate embodiment wherein multiple rounds of polymerization are performed and a restriction oligonucleotide is annealed to the newly synthesized strands, rather than to the original template;

Fig. 4 is a schematic illustration of a nested oligo annealed to a newly synthesized nucleic acid strand;

Fig. 5 is a schematic illustration of an engineered template in accordance with this disclosure;

Fig. 6 is a schematic illustration of the single primer amplification of an engineered template;

Fig. 7 shows the sequence of the nested oligo designated TMX24CMnpt;

Figs. 8a-e show the sequences of isolated Fabs produced in Example 3; and

Figs. 9a-d show the sequences of isolated Fabs produced in Example 5.

Detailed Description of Preferred Embodiments

The present disclosure provides a method of amplifying a target nucleic acid sequence. In particularly useful embodiments, the target nucleic acid sequence is a gene encoding a polypeptide or protein. The disclosure also describes how the products of the amplification may be cloned and expressed in suitable expression systems. In particularly useful embodiments, the techniques described herein are used to amplify a family of related sequences to build a complex library, such as, for example an antibody library.

The target nucleic acid sequence is exponentially amplified through a process that involves only a single primer. The ability to employ a single primer (i.e., without the need for both forward and reverse primers each having different sequences) is achieved by engineering a strand of nucleic acid that contains the target sequence to be amplified. The engineered strand of nucleic acid (sometimes referred to herein as the "engineered template") is prepared from two templates; namely, 1) a starting material that is a natural or synthetic nucleic acid (e.g., DNA or cDNA) containing the sequence to be amplified and 2) a nested oligonucleotide. The starting material can be considered the original template. The nested oligonucleotide is used as a template to extend the nucleotide sequence of the original template during creation of the engineered strand of nucleic acid. The engineered strand of nucleic acid is created from the original template by a series of manipulations that result in the presence of complementary sequences at opposite ends thereof. It is these complementary sequences that allow amplification using only a single primer.

Any nucleic acid, in purified or nonpurified form, can be utilized as the starting material for the processes described herein provided it contains or is suspected of containing the target nucleic acid sequence to be amplified. Thus, the starting material employed in the process may be, for example, DNA or RNA, including messenger RNA, which DNA or RNA may be single stranded or double stranded. In addition, a DNA-RNA hybrid which contains one strand of each may be utilized. A mixture of any of these nucleic acids may also be employed, or the nucleic acids produced from a previous amplification reaction herein using the same or different primers may be utilized. The target nucleic acid sequence to be amplified may be a fraction of a larger molecule or can be present initially as a discrete molecule. The starting nucleic acid may contain more than one desired target nucleic acid sequence which may be the same or different. Therefore, the present process may be useful not only for producing large amounts of one target nucleic acid sequence, but also for amplifying simultaneously more than one different target nucleic acid sequence located on the same or different nucleic acid molecules.

The nucleic acids may be obtained from any source, for example: genomic or cDNA libraries, plasmids, cloned DNA or RNA, or from natural DNA or RNA from any source, including bacteria, yeast, viruses, and higher organisms such as plants or animals. The nucleic acids can be naturally occurring or may be synthetic, either totally or in part. Techniques for obtaining and producing the nucleic acids used in the present invention are well known to those skilled in the art. If the nucleic acid contains two strands, it is necessary to separate the strands of the nucleic acid before it can be used as the original template, either as a separate step or simultaneously with the synthesis of the primer

extension products. Additionally, if the starting material is first strand DNA, second strand DNA may advantageously be created by processes within the purview of those skilled in the art and used as the original template from which the engineered template is created.

First strand cDNA is a particularly useful original template for the present methods. Suitable methods for generating DNA templates are known to and readily selected by those skilled in the art. In a preferred embodiment, 1st strand cDNA is synthesized in a reaction where reverse transcriptase catalyzes the synthesis of DNA complementary to any RNA starting material in the presence of an oligodeoxynucleotide primer and the four deoxynucleoside triphosphates, dATP, dGTP, dCTP, and TTP. The reaction is initiated by annealing of the oligo-deoxynucleotide primer to the 3' end of mRNA followed by stepwise addition of the appropriate deoxynucleotides as determined by base pairing relationships with the mRNA nucleotide sequence, to the 3' end of the growing chain. As those skilled in the art will appreciate, all mRNA in a sample can be used to generate first strand cDNA through the annealing of oligo dT to the polyA tail of the mRNA.

Once the original template is obtained, a primer 20 and a boundary oligonucleotide 30 are annealed to the original template 10. (See Fig. 1.) A strand of nucleic acid complementary to the portion of the original template beginning at the 3' end of the primer up to about the 5' end of the boundary oligonucleotide is polymerized.

The primer 20 that is annealed to the original template includes a first portion 22 of predetermined sequence that preferably does not anneal to the original template and a second portion 25 that anneals to the original template, and optionally includes a

restriction site 23 between the first and second portions. The primer anneals to the original template adjacent to the target sequence 12 to be amplified. It is contemplated that the primer can anneal to the original template upstream of the target sequence to be amplified, or that the primer may overlap the beginning of the target sequence 12 to be amplified as shown in Fig. 1. The predetermined sequence of the non-annealing portion 22 of the primer is not native in the original template and is selected so as to provide a sequence to which the single primer used during the amplification process can hybridize as described in detail below. Optionally, the predetermined sequence may include a restriction site useful for insertion of a portion of the engineered template into an expression vector as described more fully hereinbelow.

The boundary oligonucleotide 30 that is annealed to the original template serves to terminate polymerization of the nucleic acid. Any oligonucleotide capable of terminating nucleic acid polymerization may be utilized as the boundary oligonucleotide 30. In a preferred embodiment the boundary oligonucleotide includes a first portion 35 that anneals to the original template 10 and a second portion 32 that is not susceptible to an extension reaction. Techniques to prevent the boundary oligo from acting as a site for extension are within the purview of one skilled in the art. By way of example, portion 32 of the boundary oligo 30 may be designed so that it does not anneal to the original template 10 as shown in Fig. 1. In such embodiments, the boundary oligonucleotide 30 prevents further polymerization but does not serve as a primer for nucleic acid synthesis because the 3' end thereof does not hybridize with the original template 10. Alternatively, the 3' end of the boundary oligo 30 might be designed to include locked nucleic acid to achieve the same effect. Locked nucleic acid is disclosed for example in WO 99/14226,

the contents of which are incorporated herein by reference. Those skilled in the art will envision other ways of ensuring that no extension of the 3' end of the boundary oligo occurs.

Primers and oligonucleotides described herein may be synthesized using established methods for oligonucleotide synthesis which are well known in the art. Oligonucleotides, including primers of the present invention include linear oligomers of natural or modified monomers or linkages, such as deoxyribonucleotides, ribonucleotides, and the like, which are capable of specifically binding to a target polynucleotide by way of a regular pattern of monomer-to monomer interactions such as Watson-Crick base pairing. Usually monomers are linked by phosphodiester bonds or their analogs to form oligonucleotides ranging in size from a few monomeric units e.g., 3-4, to several tens of monomeric units. A primer is typically single-stranded, but may be double-stranded. Primers are typically deoxyribonucleic acids, but a wide variety of synthetic and naturally occurring primers known in the art may be useful for the methods of the present disclosure. A primer is complementary to the template to which it is designed to hybridize to serve as a site for the initiation of synthesis, but need not reflect the exact sequence of the template. In such a case, specific hybridization of the primer to the template depends on the stringency of the hybridization conditions. Primers may be labeled with, e.g., chromogenic, radioactive, or fluorescent moieties and used as detectable moieties.

Polymerization of nucleic acid can be achieved using methods known to those skilled in the art. Polymerization is generally achieved enzymatically, using a DNA polymerase which sequentially adds free nucleotides according to the instructions of the

template. Several different DNA polymerases are suitable for use in the present process. In a certain embodiments, the criteria for selection includes lack of exonuclease activity or DNA polymerases which do not possess a strong exonuclease . DNA polymerases with low exonuclease activity for use in the present process may be isolated from natural sources or produced through recombinant DNA techniques. Illustrative examples of polymerases that may be used, are, without limitation, T7 Sequenase v. 2.0, the Klenow Fragment of DNA polymerase I lacking exonuclease activity, the Klenow Fragment of Taq Polymerase, exo.- Pfu DNA polymerase, Vent. (exo.-) DNA polymerase, and Deep Vent. (exo-) DNA polymerase.

In a particularly useful embodiment, the use of a boundary oligonucleotide is avoided by removing unneeded portions of the starting material by digestion. In this embodiment, which is shown schematically in Fig. 2A, a restriction oligonucleotide 70 is annealed to the starting material 100 at a preselected location. The restriction oligonucleotide provides a double stranded portion on the starting material containing a restriction site 72. Suitable restriction sites, include, but are not limited to Xho I , Spe I, Nhe1, Hind III, Nco I, Xma I, Bgl II, Bst I, and Pvu I. Upon exposure to a suitable restriction enzyme, the starting material is digested and thereby shortened to remove unnecessary sequence while preserving the desired target sequence 12 (or portion thereof) to be amplified on what will be used as the original template 110. Once the original template 110 is obtained, a primer 20 is annealed to the original template 110 (see Fig. 2B) adjacent to or overlapping with the target sequence 12 as described above in connection with previous embodiments. A strand of nucleic acid 40 complementary to the portion of the original template between the 3' end of the primer 20 and the 5' end of

the original template 110 is polymerized. As those skilled in the art will appreciate, in this embodiment where a restriction oligonucleotide is employed to generate the original template, there is no need to use a boundary oligonucleotide, because primer extension can be allowed to proceed all the way to the 5' end of the shortened original template 110.

Once polymerization is complete (i.e., growing strand 40 reaches the boundary oligonucleotide 30 or the 5' end of the shortened original template 110), the newly synthesized complementary strand is separated from the original template by any suitable denaturing method including physical, chemical or enzymatic means. Strand separation may also be induced by an enzyme from the class of enzymes known as helicases or the enzyme RecA, which has helicase activity and in the presence of riboATP is known to denature DNA. The reaction conditions suitable for separating the strands of nucleic acids with helicases are described by Cold Spring Harbor Symposia on Quantitative Biology, Vol. XLIII "DNA: Replication and Recombination" (New York: Cold Spring Harbor Laboratory, 1978), B. Kuhn et al., "DNA Helicases", pp. 63-67, and techniques for using RecA are reviewed in C. Radding, Ann. Rev. Genetics, 16:405-37 (1982).

The newly synthesized complementary strand thus includes sequences provided by the primer 20 (e. g., the predetermined sequence 22, the optional restriction site 23 and the annealing portion 25 of the primer) as well as the newly synthesized portion 45 that is complementary to the portion of the original template 10 between the location at which the primer 20 was annealed to the original template 10 and either the portion of the original template 10 to which the boundary oligonucleotide 30 was annealed or the shortened 5' end of the original template. See Fig. 4.

Optionally, multiple rounds of polymerization (preferably, 15-25 rounds) using the original template and a primer are performed to produce multiple copies of the newly synthesized complementary strand for use in subsequent steps. Making multiple copies of the newly synthesized complementary strand at this point in the process (instead of waiting until the entire engineered template is produced before amplifying) helps ensure that accurate copies of the target sequence are incorporated into the engineered templates ultimately produced. It is believed that multiple rounds of polymerization based on the original template provides a greater likelihood that a better representation of all members of the library will be achieved, therefore providing greater diversity compared to a single round of polymerization.

In an alternative embodiment, newly synthesized strands are produced by annealing primer 20 as described above to original template 10 and performing multiple rounds of polymerization, without either the presence of a blocking oligonucleotide or removing a portion of the original template. In this embodiment, which is shown schematically in Fig. 3, the primer is extended along the full length of the original template to provide a full length newly synthesized strand 140. Next, a restriction oligonucleotide 170 is hybridized to the full length newly synthesized strand. The restriction oligonucleotide provides a double stranded portion on the newly synthesized strand containing a restriction site. Suitable restriction sites, include, but are not limited to Xho I , Spe I, Nhe1, Hind III, Nco I, Xma I, Bgl II, Bst I, Pvu I, Xcm I, BsaJ I, Hpa I, ApaL I, Sac I, Dra III and Sma I. Upon exposure to a suitable restriction enzyme, the newly synthesized strand is digested and thereby shortened. A nested oligonucleotide 50

can then be hybridized to the shortened newly synthesized strand 142 to complete preparation of the engineered template, as described in more detail below.

The next step in preparing the engineered template involves annealing a nested oligonucleotide 50 to the 3' end of the newly synthesized complementary strand, for example as shown in Fig. 4. As seen in Fig. 4, the nested oligonucleotide 50 provides a template for further polymerization necessary to complete the engineered template. Nested oligonucleotide 50 includes a portion 52 that does not hybridize and/or includes modified bases to the newly synthesized complementary strand, thereby preventing the nested oligonucleotide from serving as a primer. Nested oligonucleotide 50 also includes a portion 55 that hybridizes to the 3' end of the newly synthesized complementary strand. Portion 55 may be coterminous with newly synthesized portion 45 or may extend beyond newly synthesized portion 45 as shown in Fig. 4. Nested oligonucleotide 50 may optionally also include a portion 56 defining a restriction site. The final portion 58 of nested oligonucleotide 50 contains the same predetermined sequence as portion 22 of primer 20. From the point at which portion 55 extends beyond the 3' end of the beginning the newly synthesized complementary strand, the nested oligonucleotide serves as a template for further polymerization to form the engineered template. It should be understood that the nested oligo may contain part of the target sequence (if part thereof was truncated in forming the original template) or may include genes that encode a polypeptide or protein (or portion thereof) such as, for example, one or more CDR's or Framework regions or constant regions of an antibody. It is also contemplated that a collection of nested oligonucleotides having different sequences can be employed, thereby providing a variety of templates which results in a library of diverse products.

Thus, polymerization will extend the newly synthesized complementary strand by adding additional nucleic acid 60 that is complementary to the nested oligonucleotide as shown in Fig. 4. Techniques for achieving polymerization are within the purview of one skilled in the art. As previously noted, selecting a suitable polymerase, an enzyme lacking exonuclease activity may be preferred in certain embodiments.

Once polymerization is complete, the engineered template 120 is separated from the nested oligonucleotide 50 by techniques well known to those skilled in the art such as, for example, heat denaturation. The resulting engineered template 120 contains a portion derived from the original primer 20, portion 45 that is complementary to a portion of the original template, and portion 65 that is complementary to a portion of the nested oligonucleotide (see Fig. 5). Significantly, the 3' end of engineered template 120 includes portion 68 containing a sequence that is complementary to the predetermined sequence of portion 22 of primer 20. This allows for amplification of the desired sequence contained within engineered template 120 using a single primer having the same sequence as the predetermined sequence of primer portion 22 using techniques known to those of ordinary skill in the art. During single primer amplification, the presence of a polymerase having exonuclease activity is preferred because such enzymes are known to provide a "proofreading" function and have relatively higher processivity compared to polymerases lacking exonuclease activity.

Fig. 6 illustrates the steps involved in the single primer amplification of the newly synthesized cDNA template. When the primer is present in the reaction mixture it hybridizes to the sequences flanking the template and amplifies the template. When there is no primer present, it is believed that there is internal self annealing between the

5' end predetermined sequence and the 3' end sequence which is complementary to the predetermined sequence. In a preferred embodiment, the predetermined sequence and complementary predetermined sequence may be designed to anneal at higher temperatures in order to avoid miss-priming during the single primer amplification reaction .

After amplification is performed, the products may be detected using any of the techniques known to those skilled in the art. Examples of methods used to detect nucleic acids include, without limitation, hybridization with allele specific oligonucleotides, restriction endonuclease cleavage, single-stranded conformational polymorphism (SSCP), analysis.gel electrophoresis, ethidium bromide staining, fluorescence resonance energy transfer, hairpin FRET essay, and TaqMan assay.

Once the engineered nucleic acid is amplified a desired number of times, restriction sites 23 and 66 or any internal restriction sites can be used to digest the strand so that the target nucleic acid sequence can be ligated into a suitable expression vector. The vector may then be used to transform an appropriate host organism using standard methods to produce the polypeptide or protein encoded by the target sequence.

In particularly useful embodiments, the methods described herein are used to amplify target sequences encoding antibodies or portions thereof, such as, for example the variable regions (either light or heavy chain) using cDNA of an antibody. In this manner, a library of antibodies can be amplified and screened. Thus, for example, starting with antibody mRNA, first strand cDNA can be produced and digested to provide an original template. A primer can be designed to anneal upstream to a selected complementary determining region (CDR) so that the newly synthesized nucleic acid

strand includes the CDR. By way of example, if the target sequence is heavy chain CDR3, the primer may be designed to anneal to the heavy chain framework one (FR1) region. Those skilled in the art will readily envision how to design appropriate primers to anneal to other upstream sites or to reproduce other selected targets within the antibody cDNA based on this disclosure.

The following Examples are provided to illustrate, but not limit, the present invention(s):

EXAMPLE 1

Amplification of a repertoire of IgM heavy chain variable genes

1st strand cDNA synthesis and modification

Human peripheral blood lymphocyte (PBL) mRNA was used to generate traditional 1st stand cDNA with an oligo dT primer using SuperScript First-Strand Synthesis System for RT-PCR (Invitrogen Life Technologies, Carlsbad, CA) essentially according to kit instructions. The first stand cDNA product was cleaned up over a QIAGEN spin column (PCR Purification Kit from QIAGEN, Valencia, CA). A restriction oligonucleotide was added to the first strand cDNA in order to generate a double stranded DNA region that could be digested by the restriction endonuclease EcoR I. The sequence of the restriction oligonucleotide (CMEcoR I) was 5' TCC TGT GAG AAT TCC CCG TCG 3' (Seq. ID No. 1). The reaction was set up with 1st strand cDNA and 0.1uM oligonucleotide. The sample was heated to 95°C for 2 minutes and then held at 64°C for two minutes to allow specific annealing to occur. An appropriate amount of 10X restriction buffer H (Roche Diagnostics) was added to the sample and further cooled to 37°C. The restriction endonuclease EcoR I (New England Biolabs, Beverly MA) was

added and incubated at 37° C for 30 minutes. The restriction enzyme was heat inactivated at 65° C for 20 minutes and then the sample was cooled to 4°C.

2nd Strand Linear Amplification and Nested Oligo Extension

EcoR I digested 1st strand cDNA was used as the original template in a 2nd strand cDNA reaction along with primer "TMX24VH3a" (0.4 uM final), dNTPs, AmpliTaq enzyme and its 10X reaction buffer (Applied Biosystems, Foster City, CA). The primer was designed to contain the predetermined TMX24 sequence, an Xho I restriction site and a region that anneals to the 1st strand cDNA in the framework 1 region of the human antibody heavy chain genes. The sequence of "TMX24VH3a" was 5' GTG CTG GCC GTT GGA AGA GGA GTG CTC GAG GAR GTG CAG CTG GTG GAG 3' (Seq. ID No. 2) where R stands for an equal molar mixture of bases A and G. The sample was heat denatured at 95° C for 1 minute then cycled 20 times through 95° C for 5 seconds, 56° C for 10 seconds and 68° C for 1 minute. This allows linear amplification of the 2nd strand cDNA. A nested oligo designated "TMX24CM0" was then added on ice to a final concentration of 0.08 uM. The sequence of "TMX24CM0" was 5' GTG CTG GCC GTT GGA AGA GGA GTG ACT AGT AAT TCT CAC AGG AGA CGA GGG GGA 3' (Seq. ID No. 3), which contains a Spe I restriction endonuclease site to be used in subsequent cloning steps. The 3' end of the nested oligo is designed to prevent elongation by incorporation of a reverse linked (3'-3' rather than 3'-5') adenosine. The 2nd strand cDNAs were further elongated off the nested oligo by heat denaturing at 94°C for 5 seconds, then cycled 4 times for annealing and elongating at 68° C for 10 seconds and 95° for 5 seconds, followed by 68° for 30 seconds and 4°C. The resulting 2nd strand cDNA or engineered template was then cleaned up using a QIAGEN spin column (PCR

Purification Kit from QIAGEN, Valencia, CA). This step removes the oligonucleotides and allows simple buffer exchange for downstream protocols.

Single Primer Amplification (SPA)

The engineered template was amplified using Advantage 2 polymerase mix (Clontech) and its 10X reaction buffer, dNTPs, and a single primer (TMX24) having the sequence of 5' GTG CTG GCC GTT GGA AGA GGA GTG 3' (Seq. ID No. 4). The samples were heat denatured at 95°C for 1 minute then cycled 35 times through 95° for 5 seconds and 68° C for 1 minute. This was followed by an additional 3 minutes at 68° C and a 4° C hold.

Cloning and Sequencing

Amplification products of approximately 450 bp were gel purified and then digested by Xho I and Spe I and cloned into pBluescript KS+ (Stratagene). Individual clones were picked and their DNA sequence determined. All of the 16 clones analyzed were IgM heavy chain, each possessing a different CDR3 sequences of varying length thereby indicating that a diverse population of antibody chains were amplified by this method (see Table 1).

Table 1

	FR3	HCDR3	FR4
CLONE 1 (Seq. ID No.5)	YYCAR	EGSSSGAFDI	WGQ
CLONE 2 (Seq. ID No.6)	YYCAR	AAFYCSGGSCYFDYYYYGMDV	WGQ
CLONE 3 (Seq. ID No.7)	YYCAK	DIGGLGVLNFDY	WGQ
CLONE 5 (Seq. ID No.8)	YYCAK	GVLAAIRICDY	WGQ
CLONE 6 (Seq. ID No.9)	YYCAR	DPGVYDYVWGSYRYPPDAFDI	WGQ
CLONE 7 (Seq. ID No.10)	YYCAR	GMIVGATSYPDY	WGQ
CLONE 8 (Seq. ID No.11)	YYCLL	GYCSSTSCPDAFDI	WGQ
CLONE 9 (Seq. ID No.12)	YYCVI	GGAVFSGGSYRQQIDY	WGQ
CLONE 10(Seq. ID No.13)	YYCTR	DRGGSYTSHLGAFDI	WGQ
CLONE 11(Seq. ID No.14)	YYCAK	DNDLGGDYYYYGMDV	WGQ
CLONE 12(Seq. ID No.15)	YYCAR	DRRFPTDLFDI	WGQ
CLONE 13(Seq. ID No.16)	YYCAR	EDGYNSGWSYNWFDP	WGQ
CLONE 14(Seq. ID No.17)	YYCAK	DCVSGSYHYFDY	WGQ
CLONE 16(Seq. ID No.18)	YYCAK	DSYCSGGSCYYYYGVDV	WGQ
CLONE 17(Seq. ID No.19)	YYCAR	EVVPAAIIDYYYGMDV	WGQ
CLONE 18(Seq. ID No.20)	YYCAK	DLGIAVVVPAH	WGQ

EXAMPLE 2

In order to clone VH products into a vector so that the native IgM CH1 constant region could be reconstituted, a site other than the EcoR I in CH1 was utilized for the 1st strand cDNA endonuclease digestion. As those skilled in the art will appreciate, when Taq polymerase is used for this protocol, a terminal A is added to many of the newly synthesized DNA strands. In order to maximize diversity, the presence of that terminal A was taken into account in the design of the nested oligonucleotide. However, the presence of that extra A results in the loss of the EcoR I recognition site. Analysis of the IgM constant region revealed other native restriction sites that could potentially be used for this method, such as Dra III. The result of using the Dra III native restriction site in the CH1 domain is that the upstream EcoR I site remains unmodified and can be used for cloning the heavy chain repertoire. The heavy chain inserts are cloned by Xho I and

EcoR I into an appropriate vector which has the remaining IgM CH1 domain from EcoR I to the CH2 domain.

1st strand cDNA synthesis and modification

Human peripheral blood lymphocyte (PBL) mRNA was used to generate traditional 1st stand cDNA with an oligo dT primer. This was done using SuperScript First-Strand Synthesis System for RT-PCR (Invitrogen Life Technologies, Carlsbad, CA) according essentially to kit instructions. A restriction oligonucleotide was added to the first strand cDNA in order to generate a double stranded DNA region that could be digested by the restriction endonuclease Dra III. The sequence of the restriction oligonucleotide (CMDra III) was 5' GAC GAA CAC GTG GTG TGC AAA G 3' (Seq. ID No. 21). The reaction was set up with 1st strand cDNA and 1uM oligonucleotide. The sample was heated to 95°C for 2 minutes and then held at 64°C for two minutes to allow specific annealing to occur. An appropriate amount of 10X restriction buffer H (Roche Diagnostics) was added to the sample and further cooled to 37°C. The restriction endonuclease Dra III (New England Biolabs, Beverly MA) was added and incubated at 37° C for 30 minutes. The restriction enzyme was heat inactivated at 65° C for 20 minutes and then the sample was cooled to 4°C.

2nd Strand Linear Amplification and Nested Oligo Extension

Dra III digested 1st strand cDNA was used as the original template in a 2nd strand cDNA reaction along with primer "TMX24VH1a" (0.4 uM final), dNTPs, AmpliTaq enzyme and its 10X reaction buffer (Applied Biosystems, Foster City, CA). The primer was designed to contain the predetermined TMX24 sequence, an Xho I restriction site and a region that anneals to the 1st strand cDNA in the framework 1 region of the human

antibody heavy chain genes. The sequence of "TMX24VH1a" was 5'GTGCTGGCCGTTGGAAGAGGAGTGCTCGAGCAGGTKCAGCTGGTGCAG 3' (Seq. ID No. 22) where K stands for an equal molar mixture of bases G and T. The sample was heat denatured at 94° C for 1 minute then cycled 20 times through 94° C for 5 seconds, 56° C for 10 seconds and 68° C for 2 minutes. This allowed linear amplification of the 2nd strand cDNA. A nested oligo designated "TMX24CMnpt" was added on ice to a final concentration of 0.2 uM. As shown in Fig. 7, the sequence of "TMX24CMnpt" (Seq. ID No. 23) includes three 3' terminal nucleotides having modified structures which were designed to prevent elongation of the oligonucleotide. Specifically, the nested oligo has three terminal nucleotides modified with phosphorthioate and 2' OMe which is designed to prevent extension and protect against exo- and endonuclease activity. The 3' end nucleotide of this oligo is non-hybridizing (g instead of c). The 2^{nd} strand cDNAs were further elongated off the nested oligo by heat denaturing at 94°C for 1 minute, annealing and elongating at 68° C for 2 minutes, followed by 4°C. The resulting 2^{nd} strand cDNA or engineered template was then cleaned up using a QIAGEN spin column (PCR Purification Kit from QIAGEN, Valencia, CA). This step removes the oligonucleotides and allows simple buffer exchange for downstream protocols. This procedure was repeated and extended to the rest of the VH primer panel (see primer list) to generate a library of immunoglobulin products that can be cloned into an appropriate vector.

VH Framework 1 Specific Primers:

PRIMER TMX24VH1a (Seq. ID No. 25)
GTGCTGGCCGTTGGAAGAGGAGTGCTCGAGCAGGTKCAGCTGGTGCAG

PRIMER TMX24VH1b (Seq. ID No. 26)
GTGCTGGCCGTTGGAAGAGGAGTGCTCGAGCAGGTCCAGCTTGTGCAG

PRIMER TMX24VH1c (Seq. ID No. 27)
GTGCTGGCCGTTGGAAGAGGAGTGCTCGAGSAGGTCCAGCTGGTACAG

PRIMER TMX24VH1d (Seq. ID No. 28)
GTGCTGGCCGTTGGAAGAGGAGTGCTCGAGCARATGCAGCTGGTGCAG

PRIMER TMX24VH2a (Seq. ID No. 29)
GTGCTGGCCGTTGGAAGAGGAGTGCTCGAGCAGATCACCTTGAAGGAG

PRIMER TMX24VH2b (Seq. ID No. 30)
GTGCTGGCCGTTGGAAGAGGAGTGCTCGAGCAGGTCACCTTGARGGAG

PRIMER TMX24VH3a (Seq. ID No. 31)
GTGCTGGCCGTTGGAAGAGGAGTGCTCGAGGARGTGCAGCTGGTGGAG

PRIMER TMX24VH3b (Seq. ID No. 32)
GTGCTGGCCGTTGGAAGAGGAGTGCTCGAGCAGGTGCAGCTGGTGGAG

PRIMER TMX24VH3c (Seq. ID No. 33)
GTGCTGGCCGTTGGAAGAGGAGTGCTCGAGGAGGTGCAGCTGTTGGAG

PRIMER TMX24VH4a (Seq. ID No. 34)
GTGCTGGCCGTTGGAAGAGGAGTGCTCGAGCAGSTGCAGCTGCAGGAG

PRIMER TMX24VH4b (Seq. ID No. 35)
GTGCTGGCCGTTGGAAGAGGAGTGCTCGAGCAGGTGCAGCTACAGCAG

PRIMER TMX24VH5a (Seq. ID No. 36)
GTGCTGGCCGTTGGAAGAGGAGTGCTCGAGGARGTGCAGCTGGTGCAG

PRIMER TMX24VH6a (Seq. ID No. 37)
GTGCTGGCCGTTGGAAGAGGAGTGCTCGAGCAGGTACAGCTGCAGCAG

PRIMER TMX24VH7a (Seq. ID No. 38)
GTGCTGGCCGTTGGAAGAGGAGTGCTCGAGCAGGTSCAGCTGGTGCAA

In the foregoing sequences, R is an equal mixture of A and G, K is an equal mixture of G and T, and S is an equal mixture of C and G.

Single Primer Amplification (SPA)

The engineered template was amplified using Advantage 2 polymerase mix (Clontech) and its 10X reaction buffer, dNTPs and a single primer (TMX24) having the sequence 5' GTG CTG GCC GTT GGA AGA GGA GTG 3' (Seq. ID No. 4). The

samples were heat denatured at 95°C for 1 minute then cycled 30 times through 95° C for 5 seconds and 68° C for 1 minute. This was followed by an additional 3 minutes at 68°C and a 4° hold.

Cloning and Sequencing

Amplification products of approximately 450 bp are gel purified and digested by Xho I and EcoR I. The inserts are cloned into the any suitable expression vector containing the remaining portion of the IgM CH1 domain from the native EcoR I site up to, or including a portion of, the CH2 domain and a compatible restriction site for cloning the amplified fragments.

EXAMPLE 3

Construction of a phagmid display library from mRNA of a Hepatitis B positive donor.

1st strand cDNA synthesis and modification for IgG Heavy and Kappa Light Chains

Human peripheral blood lymphocyte (PBL) mRNA from a Hepatitis B vaccinated donor was used to generate traditional 1st stand cDNA with an oligo dT primer. This was done using SuperScript First-Strand Synthesis System for RT-PCR (Invitrogen Life Technologies, Carlsbad, CA) according essentially to kit instructions. Restriction oligonucleotide "CGApaL I" for IgG or "CKSac I" for kappa light chain was added to the first strand cDNA in order to generate a double stranded DNA region that could be digested by the restriction endonuclease ApaL I for IgG or Sac I for kappa light chain. "CGApaL I" sequences is 5'CCA GCG GCG TGC ACA CCT TCC3' (Seq ID No. 39). "CKSac I" sequence is 5'AGG GCC TGA GCT CGC CCG TC 3' (Seq ID No. 40). The

reaction was set up with 1st strand cDNA, 1uM oligonucleotide, and appropriate amount of 10X restriction buffer A(Roche Diagnostics). The sample was heated to 95°C for 2 minutes and then held at 64°C for two minutes to allow specific annealing to occur and cooled to 37°C. The restriction endonuclease ApaL I or Sac I (New England Biolabs, Beverly MA) was added and incubated at 37° C for 30 minutes. The restriction enzyme was heat inactivated for Sac I at 65° C for 20 minutes and then the sample was cooled to 4°C.

Digestion of the 1st strand cDNAs by each restriction endonuclease was verified by PCR amplification using techniques known to those skilled in the art. These products were not used for cloning the antibody genes. Positive amplification of the digested 1st strand cDNA was observed in reactions using the 5' VBVH1a and the 3' CG0 internal control primer for IgG and 5' VBVK1a and the 3' CK0 internal control primer for kappa. Good amplification with primers 5'VBVH1a / 3' CG0 or 5' VBVK1a/3' CK0 and minimal amplification with primers 5' VBVH1a / 3' CG1Z or 5' VK1a/3' CK1dx2 indicate successful digestion of the 1st strand cDNA template with each restriction endonuclease. Sequences of the primers used for check PCR were VBVH1a: 5' GAG CCG CAC GAG CCC CTC GAG CAG GTK CAG CTG GTG CAG 3' (Seq. ID No. 41), CG0: 5' GRG CGC CTG AGT TCC ACG ACA CCG 3' (Seq. ID No. 42), VBVK1a: 5' GAC GCG CAC AAC ACG GAG CTC RAC ATC CAG ATG ACC CAG 3' (Seq. ID No. 43), CK0: 5' GTG ACT TCG CAG GCG TAG ACT T 3' (Seq. ID No.44), CG1z: 5' GCA TGT ACT AGT TTT GTC ACA AGA TTT GGG 3' (Seq. ID No. 45), CK1dx2: 5' AGA CAG TGA GCG CCG TCT AGA ATT AAC ACT CTC CCC TGT TGA AGC TCT TTG TGA CGG GCG AAC TCA G 3' (Seq. ID No. 46).

Light Chain 2nd Strand Linear Amplification and Nested Oligo Extension

Sac I digested 1st strand cDNA was used as the original template to set up multiple 2nd strand cDNA reactions using a framework 1 specific primer (0.4 uM final), dNTPs, AmpliTaq enzyme and its 10X reaction buffer (Applied Biosystems, Foster City, CA). The primers were designed to contain predetermined TMX24K sequence 5'GAC GAC CG G CTA CCA AGA GGA GTG3' (Seq. ID No. 47) for kappa, an Xba I restriction site, and a region that annealed to 1st strand cDNA in the framework 1 region of human antibody kappa light chain genes. Those annealing sequences were derived from the VBase database primers (www.mrc-cpe.cam.ac.uk/imt-doc/public/INTRO.html) that were designed based on the known sequences of human antibodies and are reported to cover the entire human antibody repertoire of kappa light chain genes.

Kappa light Chain Framework 1 Specific Primers:

TMX24Vk1a (Seq. ID No. 48) Xba I
GACGACCGGCTACCAAGAGGAGTGTCTAGARACATCCAGATGACCCAG

TMX24Vk1b (Seq. ID No. 49)
GACGACCGGCTACCAAGAGGAGTGTCTAGAGMCATCCAGTTGACCCAG

TMX24Vk1c (Seq. ID No. 50)
GACGACCGGCTACCAAGAGGAGTGTCTAGAGCCATCCRGATGACCCAG

TMX24Vk1d (Seq. ID No. 51)
GACGACCGGCTACCAAGAGGAGTGTCTAGAGTCATCTGGATGACCCAG

TMX24Vk2a (Seq. ID No. 52)
GACGACCGGCTACCAAGAGGAGTGTCTAGAGATATTGTGATGACCCAG

TMX24Vk2b (Seq. ID No. 53)
GACGACCGGCTACCAAGAGGAGTGTCTAGAGATRTTGTGATGACTCAG

TMX24Vk3a (Seq. ID No. 54)
GACGACCGGCTACCAAGAGGAGTGTCTAGAGAAATTGTGTTGACRCAG

TMX24Vk3b (Seq. ID No. 55)
GACGACCGGCTACCAAGAGGAGTGTCTAGAGAAATAGTGATGACGCAG

TMX24Vk3c (Seq. ID No. 56)
GACGACCGGCTACCAAGAGGAGTGTCTAGAGAAATTGTAATGACACAG

TMX24Vk4a (Seq. ID No. 57)
GACGACCGGCTACCAAGAGGAGTGTCTAGAGACATCGTGATGACCCAG

TMX24Vk5a (Seq. ID No. 58)
GACGACCGGCTACCAAGAGGAGTGTCTAGAGAAACGACACTCACGCAG

TMX24Vk6a (Seq. ID No. 59)
GACGACCGGCTACCAAGAGGAGTGTCTAGAGAAATTGTGCTGACTCAG

TMX24Vk6b (Seq. ID No. 60)
GACGACCGGCTACCAAGAGGAGTGTCTAGAGATGTTGTGATGACACAG

In the foregoing sequences, R is an equal mixture of A and G, M is an equal mixture of A and C, Y is an equal mixture of C and T, W is an equal mixture of A and T, and S is an equal mixture of C and G.

The samples were heat denatured at 94° C for 1 minute then cycled 20 times through 94° C for 5 seconds, 56° C for 10 seconds, and 68° C for 2 minutes. This allowed linear amplification of the 2nd strand cDNA. A nested oligo designated "TMX24CKnpt" for kappa chains was added on ice to a final concentration of 0.2 uM. "TMX24CKnpt" contains predetermined sequenceTMX24K and the sequence was 5' GAC GAC CGG CTA CCA AGA GGA GTG CTC GAG CTC AGG CCC TGA TGG GTG ACT TCG CT 3' (Seq. ID No. 61). The 2nd strand cDNAs were further elongated off the nested oligo by heat denaturing at 94°C for 1 minute, annealing and elongating at 68° C for 2 minutes, followed by 4°C. The resulting 2nd strand cDNA (engineered template) were cleaned up using a QIAGEN spin column (PCR Purification Kit from

QIAGEN, Valencia, CA). This step removes the free oligonucleotides and allows simple buffer exchange for downstream protocols.

Light Chain Single Primer Amplification (SPA)

The engineered template was amplified using Advantage 2 polymerase mix (Clontech) and its 10X reaction buffer, dNTPs, and primer "TMX24K" for kappa chains. The sequence for "TMX24K" is 5'GAC GAC CGG CTA CCA AGA GGA GTG 3' (Seq. ID No. 62). The samples were heat denatured at 95°C for 1 minute then cycled 30 times through 95° C for 5 seconds and 68° C for 1 minute. This was followed by an additional 3 minutes at 68° C and a 4° C hold.

Light Chain Cloning

Kappa amplification products were gel purified and then digested by Xba I and Sac I. The inserts were cloned into a suitable expression vector that contains the remaining portion of the kappa light chain constant region. The ligated product was introduced into an *E. coli* by electroporation and grown overnight at 37° C. The following morning a DNA maxi prep (QIAGEN, Valencia, CA) was performed to recover the light chain library DNA. The light chain library DNA was then used in subsequent steps to clone in the heavy chain Fd fragments by Xho I / Age I to complete the construction of the library.

Heavy Chain 2nd Strand Linear Amplification and Nested Oligo Extension

ApaL I digested 1st strand cDNA was used as the original template to set up multiple 2nd strand cDNA reactions using a framework 1 specific primer (0.4 uM final), dNTPs, AmpliTaq enzyme and its 10X reaction buffer (Applied Biosystems, Foster City, CA). The primers were designed to contain the predetermined TMX24 sequence, an Xho I restriction site, and a region that annealed to 1st strand cDNA in the framework 1 region of human antibody heavy chain genes. Those annealing sequences were derived from the VBase database primers that were designed based on the known sequences of human antibodies and are reported to cover the entire human antibody repertoire of heavy chain genes.

Heavy chain Framework 1 Specific Primers:

TMX24VH1a (Seq. ID No. 63)
GTGCTGGCCGTTGGAAGAGGAGTGCTCGAGCAGGTKCAGCTGGTGCAG

TMX24VH1b (Seq. ID No. 64)
GTGCTGGCCGTTGGAAGAGGAGTGCTCGAGCAGGTCCAGCTTGTGCAG

TMX24VH1c (Seq. ID No. 65)
GTGCTGGCCGTTGGAAGAGGAGTGCTCGAGSAGGTCCAGCTGGTACAG

TMX24VH1d (Seq. ID No. 66)
GTGCTGGCCGTTGGAAGAGGAGTGCTCGAGCARATGCAGCTGGTGCAG

TMX24VH2a (Seq. ID No. 67)
GTGCTGGCCGTTGGAAGAGGAGTGCTCGAGCAGATCACCTTGAAGGAG

TMX24VH2b (Seq. ID No. 68)
GTGCTGGCCGTTGGAAGAGGAGTGCTCGAGCAGGTCACCTTGARGGAG

TMX24VH3a (Seq. ID No. 69)
GTGCTGGCCGTTGGAAGAGGAGTGCTCGAGGARGTGCAGCTGGTGGAG

TMX24VH3b (Seq. ID No. 70)
GTGCTGGCCGTTGGAAGAGGAGTGCTCGAGCAGGTGCAGCTGGTGGAG

TMX24VH3c (Seq. ID No. 71)
GTGCTGGCCGTTGGAAGAGGAGTGCTCGAGGAGGTGCAGCTGTTGGAG

TMX24VH4a (Seq. ID No. 72)
GTGCTGGCCGTTGGAAGAGGAGTGCTCGAGCAGSTGCAGCTGCAGGAG

TMX24VH4b (Seq. ID No. 73)
GTGCTGGCCGTTGGAAGAGGAGTGCTCGAGCAGGTGCAGCTACAGCAG

TMX24VH5a (Seq. ID No. 74)
GTGCTGGCCGTTGGAAGAGGAGTGCTCGAGGARGTGCAGCTGGTGCAG

TMX24VH6a (Seq. ID No. 75)
GTGCTGGCCGTTGGAAGAGGAGTGCTCGAGCAGGTACAGCTGCAGCAG

TMX24VH7a (Seq. ID No. 76)
GTGCTGGCCGTTGGAAGAGGAGTGCTCGAGCAGGTSCAGCTGGTGCAA

In the foregoing sequences, R is an equal mixture of A and G, K is an equal mixture of G and T, and S is an equal mixture of C and G.

The samples were heat denatured at 94° C for 1 minute then cycled 20 times through 94° C for 5 seconds, 56° C for 10 seconds, and 68° C for 2 minutes. This allowed linear amplification of the 2nd strand cDNA. A nested oligonucleotide designated "TMX24CGnpt" (sequence 5' GTG CTG GCC GTT GGA AGA GGA GTG TGT TTG CAC GCC GCT GGT CAG RGC GCC TGA GTT G 3' (Seq. ID No. 77)) was added on ice to a final concentration of 0.2 uM. As shown in Fig. 1 for the IgM nested oligo, the three 3' terminal nucleotides were modified to prevent oligo extension. The 2^{nd} strand cDNAs were further elongated off the nested oligo by heat denaturing at 94°C for 1 minute, annealing and elongating at 68° C for 2 minutes, followed by 4°C. The resulting 2^{nd} strand cDNA (the engineered template) was then cleaned up using a QIAGEN spin column (PCR Purification Kit from QIAGEN, Valencia, CA). This step removed the free oligonucleotides and allowed simple buffer exchange for downstream protocols.

Single Primer Amplification (SPA)

The engineered template was amplified using Advantage 2 polymerase mix (Clontech) and its 10X reaction buffer, dNTPs, and primer "TMX24". The samples was heat denatured at 95°C for 1 minute then cycled 30 times through 95° C for 5 seconds and 68° C for 1 minute. This was followed by 3 additional minutes at 68° C and a 4° C hold.

Heavy Chain Cloning & Production of the Library

The amplified products were pooled and then gel purified. DNA was recovered with QIAquick PCR purification kit (QIAGEN, Valencia, CA). The DNA was sequentially digested with Xho I and Age I restriction enzymes and then gel purified. Age I site is naturally present in the CH1 of IgG constant region upstream of ApaL I site. DNA was recovered with QIAquick Gel extraction Kit (QIAGEN, Valencia, CA).

The light chain library DNA was digested sequentially with Xho I and Age I and then gel purified. The light chain library DNA was ligated with the heavy chain fragments. Ligated DNA was placed over a spin column (PCR purification Kit , QIAGEN, Valencia, CA) to remove the reaction buffer and to concentrate the DNA. Final transformation was done in electrocompetent XL-1 Blue cells (Stratagene).

Panning and Screening of Library on HBs Ag

The library was panned on immobilized HBs Ag for 4 rounds essentially as described in Barbas III, CF, Burton, DR, Scott, JK, and Silverman, GJ (2001) Phage Display: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York. Individual clones from the 2^{nd}, 3^{rd}, and 4^{th} rounds of panning were screened by ELISA on HBs Ag.

1st Strand cDNA Synthesis and Modification for Lambda Light Chain.

Human PBL mRNA from a Hepatitis B vaccinated donor was used to generate traditional 1st strand cDNA with an oligo dT primer. This was done using SuperScript First-Strand Synthesis for RT-PCR (Invitrogen Life Technologies, Carlsbad, CA) according essentially to kit instructions. Restriction oligonucleotide "CLSma I" was added to the first strand cDNA in order to generate a double stranded DNA region that could be digested by the restriction endonuclease Sma I. "CLSma I" sequence is 5'GAC TTC TAC CCG GGA GCY GTG3' (Seq. ID No. 78) where Y is a mixture of C and T. The reaction was set up with 1st strand cDNA, 1 uM oligonucleotide, and appropriate amount of 10X restriction buffer A (Roche Diagnostics). The sample was heated to 95°C for 2 minutes and then held at 64°C for two minutes to allow specific annealing to occur and cooled to 37°C. The restriction endonuclease Sma I (New England Biolabs, Beverly MA) was added and incubated at 37°C for 30 minutes. The restriction enzyme was heat inactivated at 65°C and then the sample was cooled to 4°C.

Digestion of the 1st strand cDNA by restriction endonuclease was verified by PCR amplification using techniques known to those skilled in the art. These products were not used for cloning the antibody genes. Positive amplification of the digested 1st strand cDNA was observed in reaction using the 5'VBVL1a and 3'CL0 internal control primer. Good amplification with primers 5'VBVL1a/3'CL0 and minimal amplification with primers 5'VBVL1a/3'CL2dx2 indicated successful digestion of the 1st strand cDNA template with Sma I. Sequences of the primers for check PCR were VBVL1a 5' GAC GCG CAC A AC ACG GAG CTC CAG TCT GTG CTG ACT CAG 3' (Seq. ID No. 79), CL0 5'CCT CAG AGG AGG GYG GG A ACAG3' (Seq. ID No. 80) and CL2dx2 5'

AGA CAG TGA CGC CGT CTA GAA TTA TGA ACA TTC TGT AGG 3' (Seq. ID No. 81).

Lambda Light Chain 2nd Strand Linear Amplification and Nested Oligo Extension

Sma I digested 1st strand cDNA was used as the original template to set up multiple 2nd strand cDNA reactions using a framework 1 specific primer (0.4 uM final), dNTPs, AmpliTaq enzyme and its 10X reaction buffer (Applied Biosystems, Foster City, CA). The primers are designed to contain predetermined TMX24L sequence, an Xba I site, and a region that anneals to 1st strand cDNA in the framework region of human antibody lambda light chain genes. Those annealing sequences are derived from the VBase database primers (www.mrc-cpe.cam.ac.uk/imt-doc/public/INTRO.html) that are designed based on the known sequences of human antibodies and are reported to cover the entire human antibody repertoire of lambda light chain genes. Lambda light chain framework 1 specific primers are those used in Example 4.

The samples were heat denatured at 94°C for 1 minute and then cycled 20 times through 94°C for 5 seconds, 56°C for 10 seconds, and 68°C for 2 minutes. This allowed linear amplification of the 2nd strand cDNA. A nested oligo nucleotide designated "TMX24CLnpt" as shown in Example 4 was added on ice to a final concentration of 0.2 uM. As shown in Fig. 7 for the IgM nested oligonucleotide "TMX24CMnpt", the 3' terminal nucleotides of "TMX24CLnpt" are modified to prevent oligo extension. The 2nd strand cDNAs were further elongated off the nested oligonucleotide by heat denaturing at 94°C for 1 minutes, annealing and elongating at 68°C for 2 minutes, followed by 4°C. The resulting 2nd strand cDNAs (the engineered template) were cleaned up using PCR

Purification Kit (QIAGEN, Valencia, CA). This step removes the free oligonucleotides and allows simple buffer exchange for downstream protocols.

Lambda Light Chain Single Primer Amplification (SPA)

The engineered template was amplified using Advantage 2 polymerase mix (Clontech) and its 10x reaction buffer, dNTPs, and primer "TMX24L". The predetermined sequence of TMX24L is 5'GAC GAC CGG CTA CCA AGA GGA CAG3' (Seq. ID No. 82). The samples were heat denatured at 95°C for 1 minutes then cycled 30 times through 95°C for 5 seconds and 68°C for 1 minute. This was followed by an additional 3 minutes at 68°C and a 4°C hold.

Lambda Light Chain Cloning

Lambda light chain amplification products were cleaned up by PCR purification kit (QIAGEN, Valencia, CA) and digested by Xba I and Sac I. The insert was gel purified using a gel extraction kit (QIAGEN, Valencia, CA) and cloned into an appropriate vector that contains the remaining portion of the lambda light chain constant region. The ligated product was introduced into an E. coli by electroporation and grown overnight at 37°C. The following morning a DNA maxi prep (QIAGEN, Valencia, CA) was performed to recover the lambda light chain library DNA.

Heavy Chain Cloning & Production of the IgG Lambda Library

The lambda light chain library DNA prepared above was sequentially digested by Xho I and Age I for the insertion of the heavy chain Fd fragments prepared also for the IgG kappa library as described previously. The ligated product was then introduced into an E. coli by electroporation and grown overnight at 37°C. The following morning a DNA

maxi prep (QIAGEN, Valencia, CA) was performed to recover the complete IgG lambda library DNA.

Panning and Screening of Library on HBs Ag

The panning and screening was performed as described previously for IgG kappa library.

DNA Sequencing Analysis and Characterization of Isolated Fabs

Clones that showed specific binding to HBsAg and minimal binding to a non-specific protein, ovalbumin by ELISA screening were analyzed by DNA sequencing. See Figs. 8a-e. Total of 38 distinct IgG kappa Fabs (25 heavy chains and 37 light chains) and 17 distinct IgG lambda Fabs (13 heavy chains and 16 light chains) to HBsAg were isolated from the libraries made from the PBL mRNA from a Hepatitis B vaccinated donor.

EXAMPLE 4

Construction of a phage display antibody library from human PBL mRNA.

1st strand cDNA Synthesis and Modification for Light Chains

Human PBL mRNA from donor was is to generate traditional 1st stand cDNA with an oligo dT primer using SuperScript First-Strand Synthesis System for RT-PCR (Invitrogen Life Technologies, Carlsbad, CA) essentially according to kit instructions. Kappa and lambda light chain reactions are set up separately. Restriction oligonucleotide "CKSac I" or "CLSma I" is added to the first strand cDNA in order to generate a double stranded DNA region that could be digested by the restriction endonuclease Sac I for kappa or Sma I for lambda light chains. As there are multiple lambda constant regions (C1, C2, C3, and C6) it is important to note that the Sma I site is conserved among all functional lambda constant domains (C1, C2, C3, and C6). "CKSac I" sequence is

5'AGG GCC TGA GCT CGC CCG TC 3' (Seq ID No. 179), "CLSma I" sequence is 5' GAC TTC TAC CCG GGA GCY GTG 3' (Seq ID No. 180) where Y is a mixture of C and T. The reactions are set up with 1st strand cDNA and 1uM oligonucleotide. The sample is heated to 95°C for 2 minutes and then held at 64°C for two minutes to allow specific annealing to occur. An appropriate amount of 10X restriction buffer A (Roche Diagnostics) is added to the samples and further cooled to 37°C. The restriction endonuclease Sac I or Sma I (New England Biolabs, Beverly MA) is added and incubated at 37° C for 30 minutes. The restriction enzyme is heat inactivated at 65° C for 20 minutes and then the sample is cooled to 4°C.

Light Chain 2nd Strand Linear Amplification and Nested Oligo Extension

Sac I digested kappa 1st strand cDNA or Sma I digested lambda 1st strand cDNA are used as the original templates to set up multiple 2nd strand cDNA reactions using a framework 1 specific primer (0.4 uM final), dNTPs, AmpliTaq enzyme and its 10X reaction buffer (Applied Biosystems, Foster City, CA). The primers are designed to contain TMX24K (for kappa) or TMX24L (for lambda) sequence, an Xba I restriction site, and a region that annealed to 1st strand cDNA in the framework 1 region of human antibody kappa or lambda chain genes. Those annealing sequences are derived from the VBase database primers (www.mrc-cpe.cam.ac.uk/imt-doc/public/INTRO.html) that are designed based on the known sequences of human antibodies and are reported to cover the entire human antibody repertoire of light chain genes. Kappa light chain framework 1 specific primers are those used in Example 3. See the following list of primers for use in lambda amplification.

Lambda light chain Framework 1 Specific Primers:

TMX24VL1a (Seq. ID No. 181)
GACGACCGGCTACCAAGAGGACAGTCTAGACAGTCTGTGCTGACTCAG

TMX24VL1b (Seq. ID No. 182)
GACGACCGGCTACCAAGAGGACAGTCTAGACAGTCTGTGYTGACGCAG

TMX24VL1C (Seq. ID No. 183)
GACGACCGGCTACCAAGAGGACAGTCTAGACAGTCTGTCGTGACGCAG

TMX24VL2 (Seq. ID No. 184)
GACGACCGGCTACCAAGAGGACAGTCTAGACAGTCTGCCCTGACTCAG

TMX24VL3a (Seq. ID No. 185)
GACGACCGGCTACCAAGAGGACAGTCTAGATCCTATGWGCTGACTCAG

TMX24VL3b (Seq. ID No. 186)
GACGACCGGCTACCAAGAGGACAGTCTAGATCCTATGAGCTGACACAG

TMX24VL3c (Seq. ID No. 187)
GACGACCGGCTACCAAGAGGACAGTCTAGATCTTCTGAGCTGACTCAG

TMX24VL3d (Seq. ID No. 188)
GACGACCGGCTACCAAGAGGACAGTCTAGATCCTATGAGCTGATGCAG

TMX24VL4 (Seq. ID No. 189)
GACGACCGGCTACCAAGAGGACAGTCTAGACAGCYTGTGCTGACTCAA

TMX24VL5 (Seq. ID No. 190)
GACGACCGGCTACCAAGAGGACAGTCTAGACAGSCTGTGCTGACTCAG

TMX24VL6 (Seq. ID No. 191)
GACGACCGGCTACCAAGAGGACAGTCTAGAAATTTTATGCTGACTCAG

TMX24VL7 (Seq. ID No. 192)
GACGACCGGCTACCAAGAGGACAGTCTAGACAGRCTGTGGTGACTCAG

TMX24VL8 (Seq. ID No. 193)
GACGACCGGCTACCAAGAGGACAGTCTAGACAGACTGTGGTGACCCAG

TMX24VL4/9 (Seq. ID No. 194)
GACGACCGGCTACCAAGAGGACAGTCTAGACWGCCTGTGCTGACTCAG

TMX24VL10 (Seq. ID No. 195)
GACGACCGGCTACCAAGAGGACAGTCTAGACAGGCAGGGCTGACTCAG

In the foregoing sequences, R is an equal mixture of A and G, M is an equal mixture of A and C, Y is an equal mixture of C and T, W is an equal mixture of A and T, and S is an equal mixture of C and G.

The samples are heat denatured at 94° C for 1 minute then cycled 20 times through 94° C for 5 seconds, 56° C for 10 seconds, and 68° C for 2 minutes. This allowed linear amplification of the 2nd strand cDNA. A nested oligonucleotide designated "TMX24CKnpt" for kappa chains or "TMX24CLnpt" for lambda chains are added on ice to a final concentration of 0.2 uM. The nested oligonucleotide sequences are; "TMX24CKnpt" 5' GAC GAC CGG CTA CCA AGA GGA GTG CTC GAG CTC AGG CCC TGA TGG GTG ACT TCG CT 3' (Seq. ID No. 196) and "TMX24CLnpt" 5' GAC GAC CGG CTA CCA AGA GGA CAG AAG AGC TCC TGG GTA GAA GTC ACT KAT SAG RCA CAG 3' (Seq. ID No. 197). As shown in Fig. 7 for the IgM nested oligo, the three 3' terminal nucleotides are modified to prevent oligo extension. The 2^{nd} strand cDNAs are further elongated off the nested oligos by heat denaturing at 94°C 1 minute, annealing and elongating at 68° C for 2 minutes, followed by 4°C. The resulting 2^{nd} strand cDNA (the engineered templates) are purified using a QIAGEN spin column (PCR Purification Kit from QIAGEN, Valencia, CA). This step removes the free oligonucleotides and allows simple buffer exchange for downstream protocols.

Light Chain Single Primer Amplification (SPA)

The engineered template is amplified using Advantage 2 polymerase mix (Clontech) and its 10X reaction buffer, dNTPs, and primer "TMX24K" for kappa chains, or "TMX24L" for lambda chains. The sequence for "TMX24K" is 5'GAC GAC CGG CTA CCA AGA GGA GTG 3' (Seq. ID No. 198), and for "TMX24L" it is 5' GAC GAC CGG CTA CCA AGA GGA CAG 3' (Seq. ID No. 199). The samples are heat denatured at 95°C for 1 minute then cycled 30 times through 95° C for 5 seconds and 68° C for 1 minute. This is followed by an additional 3 minutes at 68° C and a 4° C hold.

Light Chain Cloning

Kappa and Lambda amplification products were cleaned using a PCR purification kit (QUIAGEN) and were separately gel purified. Those products are digested by Xba I and Sac I. The inserts are cloned into an appropriate vector that contains the remaining portion of the respective light chain constant region. The ligated product is introduced into *E. coli* by electroporation and grown overnight at 37° C. The following morning a DNA maxiprep is performed to recover the light chain library DNA. The light chain library DNA preps are used as the cloning vector for insertion of the heavy chain Fd fragments by Xho I / EcoR I to complete the construction of the library.

1st strand cDNA Synthesis and Modification for Heavy Chains

Human PBL mRNA from a donor is used to generate traditional 1st stand cDNA with an oligo dT primer. This is done using SuperScript First-Strand Synthesis System for RT-PCR (Invitrogen Life Technologies, Carlsbad, CA) according essentially to their instructions. Restriction oligonucleotide CMDra III is added to the first strand cDNA in order to generate a double stranded DNA region that could be digested by the restriction endonuclease Dra III. The reaction is set up with 1st strand cDNA and 1uM oligonucleotide. The sample is heated to 95°C for 2 minutes and then held at 64°C for two minutes to allow specific annealing to occur. An appropriate amount of 10X restriction buffer H (Roche Diagnostics) is added to the sample and further cooled to 37°C. The restriction endonuclease Dra III (New England Biolabs, Beverly MA) is added and incubated at 37° C for 30 minutes followed by cooling at 4° C.

Digestion of the 1st strand cDNAs by Dra III is verified by PCR amplification. Amplification products will not be used for cloning antibody fragments. Positive

amplification of the digested 1st strand cDNA is observed in reactions using the 5' VBVH1a and the 3' CM0 internal control primer under two different buffer conditions. Good amplification with primers 5'VBVH1a / 3' CM0 and minimal amplification with primers 5' VBVH1a / 3' CM1 indicate successful Dra III digestion of the 1st strand cDNA template.

Heavy Chain 2nd Strand Linear Amplification and Nested Oligo Extension

Dra III digested 1st strand cDNA is used as the original template to set up multiple 2nd strand cDNA reactions using a framework 1 specific primer (0.4 uM final), dNTPs, AmpliTaq enzyme and its 10X reaction buffer (Applied Biosystems, Foster City, CA). The primers are designed to contain the TMX24 sequence, an Xho I restriction site, and a region that annealed to 1st strand cDNA in the framework 1 region of human antibody heavy chain genes. Those annealing sequences are derived from the VBase database primers that are designed based on the known sequences of human antibodies and are reported to cover the entire human antibody repertoire of heavy chain genes as described above in example 3. Heavy chain framework 1 specific primers used are those as listed in example 3.

The samples are heat denatured at 94° C for 1 minute then cycled 20 times through 94° C for 5 seconds, 56° C for 10 seconds, and 68° C for 2 minutes. This allowed linear amplification of the 2nd strand cDNA. A nested oligo nucleotide designated "TMX24CMnpt" (as used in Example 3) is added on ice to a final concentration of 0.2 uM. The 2nd strand cDNAs are further elongated off the nested oligo by heat denaturing at 94°C for 1 minute, annealing and elongating at 68° C for 2 minutes, followed by 4°C. The resulting 2nd strand cDNA (engineered template) is then cleaned

up using a QIAGEN spin column (PCR Purification Kit from QIAGEN, Valencia, CA). This step removed the free oligonucleotides and allowed simple buffer exchange for downstream protocols.

Heavy Chain Single Primer Amplification (SPA)

The engineered template is amplified using Advantage 2 polymerase mix (Clontech) and its 10X reaction buffer, dNTPs, and primer "TMX24". The samples are heat denatured at 95°C for 1 minute then cycled 30 times through 95° C for 5 seconds and 68° C for 1 minute. This is followed by 3 additional minutes at 68° C and a 4° C hold.

Heavy Chain Cloning & Production of the Library

Amplification products of approximately 500 bp are gel purified and then digested by Xho I and EcoR I. The inserts are cloned into an appropriate vector contains the remaining portion of the IgM CH1 domain. The ligated product containing a Fab library is introduced into *E. coli* by electroporation.

In order to produce the Fab library on the surface of bacteriophage, a suppressor strain of cells such as XL1BLUE (Stratagene) is used. Following electroporation, the cells are shaken for 1 hour at 37° then carbenicillin is added to 20 ug/ml. After one hour shaking at 37° C the carbenicillin is increased to 50 ug/ml for an additional hour at 37° C. VCS-M13 helper phage (Stratagene) are then added to provide all the necessary components for generation of phagemid particles and the volume of the culture is increased to 100mls of SB media. After an hour at 37°C kanamycin is added to 70 ug/ml to select for those bacteria containing helper phage DNA. The culture is shaken at 37° overnight. During that time the bacteria produce new phagemid particles that have Fab

displayed on its surface. The following morning the phagemid particles can be isolated by spinning out the bacterial cells and then precipitating the phagemid particles from the supernate with 4% PEG 8000 and 0.5 M NaCl on ice for 30 minutes. Precipitated phage pellet on centrifugation at 14,300 Xg. The pellet can be resuspended in PBS/1%BSA. The preparation can be filtered to remove bacterial debris. The resulting library is stored at 4°.

EXAMPLE 5

Construction of a phagemid display library from mRNA of mice immunized with IgE or a recombinant IgE Fc CH2~4.

1st strand cDNA synthesis and modification for IgG Heavy and Kappa Light Chains

Mouse spleen mRNA from mice immunized with human IgE or recombinant human IgE was used to generate traditional 1st strand cDNA with an oligo dT primer. This was done using SuperScript First-Strand Synthesis for RT-PCR (Invitrogen Life Technologies, Carlsbad, CA) according essentially to kit instructions. Restriction oligonucleotide "mCG1Xcm I" for IgG1, "mCG2aBsaJ I" for IgG2a, or "mCKHpa I" for kappa light chain was added to the first strand cDNA in order to generate a double stranded DNA region that could be digested by the restriction endonuclease Xcm I for IgG1, BsaJ I for IgG2a, or Hpa I for kappa light chain. "mCG1Xcm I" sequences is 5'CTAACTCCAT GGTGACCCTGGGATG3' (Seq. ID No. 200). "mCG2aBsaJ I" sequence is 5'CAACTGGCTCCTCGGT GACTCTAG3' (Seq. ID No. 201), "mCKHpa I" sequence is 5'CAGTGAGCAGTTAACATCTGGAGG3' (Seq. No. 202). The reaction was set up with 1st strand cDNA 1uM oligonucleotide, and appropriate amount of 10x NEBuffer (New England Biolabs, Beverly MA) or 10X restriction buffer A(Roche

Diagnostics). The sample was heated to 95°C for 2 minutes and then held at 64°C for two minutes to allow specific annealing to occur and cooled to 37°C for Xcm I and Hpa I and 60 °C for BsaJ I. The restriction endonuclease Xcm I, BsaJ I, or Hpa I (New England Biolabs, Beverly MA) was added and incubated at 37°C for 30 minutes, 60 °C for 30 min, and 37°C for 10 minutes, respectively. The restriction enzyme was heat inactivated for Xcm I at 65°C for 20 minutes and for BsaJ I at 80°C for 20 min and then the sample was cooled to 4°C.

Digestion of the 1st strand cDNAs by each restriction endonuclease was verified by PCR amplification using techniques known to those skilled in the art. These products were not used for cloning the antibody genes. Positive amplification of the digested 1st strand cDNA was observed in reactions using the 5' TMX24mVHIIBshort and the 3' mCG1 internal control primer for IgG1, 5' TMX24mVHIIBshort and the 3' mCG2a internal control primer for IgG2a, and 5' TMX24mVKIVshort and the 3' mCK0 internal control primer for kappa. Good amplification with primers 5' TMX24mVHIIBshort / 3' mCG1 or primers 5' TMX24mVHIIBshort / 3' mCG2a or 5' TMX24mVKIVshort /3' mCK0 and minimal amplification with primers 5' TMX24mVHIIBshort / 3' mCG1B or 5' TMX24mVHIIBshort / 3' mCG2aB or 5' TMX24mVKIVshort /3' mCKB indicate successful digestion of the 1st strand cDNA template with each restriction endonuclease. Sequences of the primers used for check PCR were

TMX24mVHIIBshort (Seq. ID No. 203)
5'GACGTGGCCGTTGGAAGAGGAGTGCTCGAGGTCCAACTGCAGCAGYC3'
mCG1 (Seq. ID No. 204) 5'CATGGAGTTAGTTTGGGCAGCAG3'
mCG1B (Seq. ID No. 205) 5'CAACGTTGCAGGTGACGGTCTC3'

mCG2a (Seq. ID No. 206) 5'CGAGGAGCCAGTTGTATCTCCAC3'

mCG2aB (Seq. ID No. 207) 5'CCACATTGCAGGTGATGGACTG3'

TMX24mVKIVshort (Seq. ID No. 208)

5'GACGACCGGCTACCAAGAGGAGTGTCTAGAGAAAWTGTGCTCACCCAGTC TC3'

mCK0 (Seq. ID No. 209) 5'CTGCTCACTGGATGGTGGGAAG3'

mCKB (Seq. ID No. 210) 5'GAGTGGCCTCACAGGTATAGCTG3'

Light Chain 2nd Strand Linear Amplification and Nested Oligo Extension

Hpa I digested 1st strand cDNA was used as the original template to set up multiple 2nd strand cDNA reactions using a framework 1 specific primer (0.4 uM final), dNTPs, AmpliTaq enzyme and its 10X reaction buffer (Applied Biosystems, Foster City, CA). The primers were designed to contain TMX24mK sequence for kappa, and Xba I restriction site, and a region that annealed to 1st strand cDNA in the framework 1 region of mouse antibody kappa light chain genes. Those annealing sequences were designed based on the known sequences of mouse antibodies derived from Kabat database (http://immuno.bme.nwu.edu/) to cover the entire mouse antibody repertoire of kappa light chain genes.

D. Kappa Framework 1 Specific Primers:

TMX24mVKIshort(Seq. ID No. 211)Xba I
5'GACGACCGGCTACCAAGAGGAGTGTCTAGAGACATTGTGATGWCACAGTCTC3'
TMX24mVKIIashort (Seq. ID No. 212)
5'GACGACCGGCTACCAAGAGGAGTGTCTAGAGATGTTKTGATGACCCARACTC3'
TMX24mVKIIbshort (Seq. ID No. 213)
5'GACGACCGGCTACCAAGAGGAGTGTCTAGAGACATTGTGATGACKCAGGCTG3'
TMX24mVKIIIshort (Seq. ID No. 214)
5'GACGACCGGCTACCAAGAGGAGTGTCTAGAGACAWTGTGCTGACCCARTCTC3'
TMX24mVKIVshort (Seq. ID No. 215)
5'GACGACCGGCTACCAAGAGGAGTGTCTAGAGAAAWTGTGCTCACCCAGTCTC3'
TMX24mVKVashort (Seq. ID No. 216)
5'GACGACCGGCTACCAAGAGGAGTGTCTAGAGACATCCAGATGACMCAGTCTC3'
TMX24mVKVbshort (Seq. ID No. 217)
5'GACGACCGGCTACCAAGAGGAGTGTCTAGAGATATCCAGATGACACAGACTAC3'
TMX24mVKVcshort (Seq. ID No. 218)
5'GACGACCGGCTACCAAGAGGAGTGTCTAGAGACATTGTSATGACCCAGTC3'
TMX24mVKVIshort (Seq. ID No. 219)
5'GACGACCGGCTACCAAGAGGAGTGTCTAGACAAATTGTTCTCACCCAGTCTC3'

Wherein (R is and equal mixture of A and G, M is and equal mixture of A and C, K is and equal mixture of G and T, W is and equal mixture of A and T, and S is and equal mixture of C and G).

The samples were heat denatured at 94° C for 1 minute then cycled 20 times through 94° C for 5 seconds, 56° C for 10 seconds, and 68° C for 2 minutes. This allowed linear amplification of the 2nd strand cDNA. A nested oligo designated "TMX24mCKnoer" for kappa chains was added on ice to a final concentration of 0.2 uM. The sequence of; "TM24CKnpt" was 5'GACGACCGGCTACCAAGAGGAGTGTCCG GATGTTAACTGCTCACTGGATGGTGGGAAGATGG2'OMe[A(ps)U(ps)U(ps)](propyl) 3' (Seq. ID No. 220). The 2nd strand cDNAs were further elongated off the nested oligo by heat denaturing at 94°C for 1 minute, annealing and elongating at 68° C for 2 minutes, followed by 4°C. The resulting 2nd strand cDNA (engineered template) were cleaned up using a QIAGEN spin column (PCR Purification Kit from QIAGEN,

Valencia, CA). This step removes the free oligonucleotides and allows simple buffer exchange for downstream protocols.

Light Chain Single Primer Amplification (SPA)

The engineered template was amplified using Advantage 2 polymerase mix (Clontech) and its 10X reaction buffer, dNTPs, and primer "TMX24mK" for kappa chains. The sequence for "TMX24mK" is 5'GACGACCGGCTACCAAGAGGAGTG3' (Seq. ID No. 221). The samples were heat denatured at 95°C for 1 minute then cycled 25times through 95° C for 5 seconds and 68° C for 1 minute. This was followed by an additional 3 minutes at 68° C and a 4° hold.

Light Chain Cloning

Kappa amplification products were gel purified and then digested by Xba I and BspE I. The inserts were cloned into a suitable expression vector that contains the remaining portion of the kappa light chain constant region. The ligated product was introduced into E. coli by electroporation and grown overnight at 37° C. The following morning a DNA maxiprep was performed to recover the light chain library DNA. The light chain library DNA was used in subsequent steps to clone in the heavy chain Fd fragments by Xho I / Bln I to complete the construction of the library as described below in Heavy Chain Cloning.

Heavy Chain 2nd Strand Linear Amplification and Nested Oligo Extension

Xcm I and BsaJ I digested 1st strand cDNAs were used to set up multiple 2nd strand cDNA reactions using framework 1 specific primer (0.4 uM final), dNTPs, AmpliTaq enzyme and its 10X reaction buffer (Applied Biosystems, Foster City, CA). The primers were designed to contain the TMX24mH sequence, an Xho I restriction site,

and a region that annealed to 1st strand cDNA in the framework 1 region of mouse antibody heavy chain genes. Those annealing sequences were designed based on the known sequences of mouse antibodies derived from Kabat database (http://immuno.bme.nwu.edu/) to cover the entire mouse antibody repertoire of heavy chain genes.

Heavy Chain Framework 1 Specific Primers:

TMX24mVHIAshorter(Seq. ID No. 222) Xho I
5'GACGTGGCCGTTGGAAGAGGAGTGCTCGAGGTGCAGCTTCAGSAGTC3'

TMX24mVHIBshorter (Seq. ID No. 223)
5'GACGTGGCCGTTGGAAGAGGAGTGCTCGAGGTGCAGCTGAAGSAGTC3'

TMX24mVHIIAshorter (Seq. ID No. 224)
5'GACGTGGCCGTTGGAAGAGGAGTGCTCGAGGTYCAGCTGCARCARTC3'

TMX24mVHIIBshorter (Seq. ID No. 225)
5'GACGTGGCCGTTGGAAGAGGAGTGCTCGAGGTCCAACTGCAGCAGYC3'

TMX24mVHIICshorter (Seq. ID No. 226)
5'GACGTGGCCGTTGGAAGAGGAGTGCTCGAGGTTCAGCTGCAGCAGTC3'

TMX24mVHIIIAshorter (Seq. ID No. 227)
5'GACGTGGCCGTTGGAAGAGGAGTGCTCGAGGTGAAGCTGGTGGAGWC3'

TMX24mVHIIIBshorter (Seq. ID No. 228)
5'GACGTGGCCGTTGGAAGAGGAGTGCTCGAGGTGAAGCTTCTGGAGTC3'

TMX24mVHIIIDshorter (Seq. ID No. 229)
5'GACGTGGCCGTTGGAAGAGGAGTGCTCGAGGTGMAGCTGGTGGAGTC3'

Wherein (R is an equal mixture of A and G, M is an equal mixture of A and C, Y is an equal mixture of C and T, and S is an equal mixture of C and G).

The samples were heat denatured at 94° C for 1 minute then cycled 20 times through 94° C for 5 seconds, 56° C for 10 seconds, and 68° C for 2 minutes. This allowed linear amplification of the 2nd strand cDNA. A nested oligo designated "TMX24mCG1noer" for IgG1 and "TMX24mCG2anoer" for IgG2a was added on ice to

a final concentration of 0.2 uM. The sequence of; "TMX24mCG1noer" was 5'GACGTGGCCGTTGGAAGAGGAGTGCCTAGGGTTACCATGGAGTTAGTTTGG GCAGCAGA2'OMe[U(ps)C(ps)A(ps)](propyl) 3' (Seq. ID No. 230) and "TMX24mCG2anoer" was 5'GACGTGGCCGTTGGAAGAGGAGTGCCTAGGGTCATCGAGGAGCCAGTTGTA TCTCCACA2'OMe[C(ps)A(ps)U(ps)](propyl) 3' (Seq. ID No. 231).

The 2nd strand cDNAs were further elongated off the nested oligo by heat denaturing at 94°C for 1 minute, annealing and elongating at 68° C for 2 minutes, followed by 4°C. The resulting 2nd strand cDNA (engineered template) were cleaned up using a QIAGEN spin column (PCR Purification Kit from QIAGEN, Valencia, CA). This step removes the free oligonucleotides and allows simple buffer exchange for downstream protocols.

Heavy Chain Single Primer Amplification (SPA)

The engineered template was amplified using Advantage 2 polymerase mix (Clontech) and its 10X reaction buffer, dNTPs, and primer "TMX24mH" for heavy chains. The sequence for "TMX24mH" is 5' GACGTGGCCGTTGGAAGAGGAGTG 3' (Seq. ID No. 232). The samples were heat denatured at 95°C for 1 minute then cycled 28 times for IgG1 and 30 times for IgG2a through 95° C for 5 seconds and 68° C for 1 minute. This was followed by an additional 3 minutes at 68° C and a 4° hold.

Heavy Chain Cloning

Heavy chain amplification products were gel purified and then digested by Xho I and Bln I. The inserts were cloned into kappa chain library DNAs that contain the remaining portion of the heavy chain constant region for IgG1 and IgG2a. The ligated

product was introduced into E. coli by electroporation and grown overnight at 37° C. The following morning a DNA maxiprep was performed to recover the IgG1 kappa or IgG2a kappa library DNA.

Panning and Screening of Libraries on recombinant IgE Fc CH2~4

The libraries panned on recombinant IgE Fc CH2~4 for 4 rounds essentially as described in Barbas III, CF Burton, DR, Scott, JK, and Silverman, GJ (2001) Phage Display: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York. Individual clones from the 2nd, 3rd, and 4th rounds of panning were screened by ELISA on recombinant IgE Fc CH2~4.

Clones that showed specific binding to IgE IgE Fc CH2~4 and minimal binding to a non-specific protein, ovalbumin by ELISA were analyzed by DNA sequencing. A total of 31 distinct Fabs to IgE Fc CH2~4 were isolated from mice libraries. See Figs. 9a-d.

Example 6

Construction of IgA antibody libraries

1st strand cDNA synthesis and modification

Human peripheral blood lymphocyte (PBL) mRNA are used to generate traditional 1st stand cDNA with an oligo dT primer. This is done using SuperScript II RT cDNA Synthesis Kit (Invitrogen Life Technologies, Carlsbad, CA) according essentially to their instructions. Restriction oligonucleotide "CABsrG I" is added to the first strand cDNA in order to generate a double stranded DNA region that can be digested by the restriction endonuclease BsrG I. The sequence of "CABsrG I" is 5' TCC GGG GAC CTG TAC ACC ACG AGC AG 3' (SEQ ID NO 279). The reaction is set up with 1st

strand cDNA and 0.1μM oligonucleotide. The sample is heated to 95°C for 2 minutes and then held at 64°C for 2 minutes to allow specific annealing to occur. An appropriate amount of 10X restriction buffer 2 (New England Biolabs, Beverly MA) is added to the sample and further cooled to 37°C. The restriction endonuclease BsrG I (New England Biolabs, Beverly MA) is added and incubated at 37° C for 30 minutes. The restriction enzyme is heat inactivated at 80° C for 20 minutes and then the sample is cooled to 4°C.

2nd strand cDNA synthesis and nested oligonucleotide extension reaction (NOER)

BsrG I digested 1st strand cDNA is used to set up multiple 2nd strand cDNA reactions using framework 1 specific primers (0.4 μM final), dNTPs, AmpliTaq enzyme and its 10X reaction buffer (Applied Biosystems, Foster City, CA). The primers, which are listed below in Table A, are designed to contain the TMX24 sequence, an Xho I restriction site, and a region that anneals to 1st strand cDNA in the framework 1 region of human antibody heavy chain genes. Those annealing sequences are derived from the Vbase database primers that were designed based on the known sequences of human antibodies and are reported to cover the entire human repertoire of heavy chain genes.

TABLE A

Framework 1 Specific Primers:

TMX24VH1a (SEQ ID NO 280)

GTGCTGGCCGTTGGAAGAGGAGTGCTCGAGCAGGTKCAGCTGGTGCAG

TMX24VH1b (SEQ ID NO 281)

GTGCTGGCCGTTGGAAGAGGAGTGCTCGAGCAGGTCCAGCTTGTGCAG

TMX24VH1c (SEQ ID NO 282)

GTGCTGGCCGTTGGAAGAGGAGTGCTCGAGSAGGTCCAGCTGGTACAG

TMX24VH1d (SEQ ID NO 283)

GTGCTGGCCGTTGGAAGAGGAGTGCTCGAGCARATGCAGCTGGTGCAG

TMX24VH2a (SEQ ID NO 284)

GTGCTGGCCGTTGGAAGAGGAGTGCTCGAGCAGATCACCTTGAAGGAG

TMX24VH2b (SEQ ID NO 285)

GTGCTGGCCGTTGGAAGAGGAGTGCTCGAGCAGGTCACCTTGARGGAG

TABLE A (Cont'd)

TMX24VH3a (SEQ ID NO 286)

GTGCTGGCCGTTGGAAGAGGAGTGCTCGAGGARGTGCAGCTGGTGGAG

TMX24VH3b (SEQ ID NO 287)

GTGCTGGCCGTTGGAAGAGGAGTGCTCGAGCAGGTGCAGCTGGTGGAG

TMX24VH3c (SEQ ID NO 288)

GTGCTGGCCGTTGGAAGAGGAGTGCTCGAGGAGGTGCAGCTGTTGGAG

TMX24VH4a (SEQ ID NO 289)

GTGCTGGCCGTTGGAAGAGGAGTGCTCGAGCAGSTGCAGCTGCAGGAG

TMX24VH4b (SEQ ID NO 290)

GTGCTGGCCGTTGGAAGAGGAGTGCTCGAGCAGGTGCAGCTACAGCAG

TMX24VH5a (SEQ ID NO 291)

GTGCTGGCCGTTGGAAGAGGAGTGCTCGAGGARGTGCAGCTGGTGCAG

TMX24VH6a (SEQ ID NO 292)

GTGCTGGCCGTTGGAAGAGGAGTGCTCGAGCAGGTACAGCTGCAGCAG

TMX24VH7a (SEQ ID NO 293)

GTGCTGGCCGTTGGAAGAGGAGTGCTCGAGCAGGTSCAGCTGGTGCAA

In each of the foregoing sequences, R is A or G, K is G or T, and S is C or G.

The sample is heat denatured at 94° C for 1 minute then cycled 20 times through 94°C for 5 seconds, 56°C for 10 seconds, and 68°C for 2 minutes. This allows linear amplification of the 2nd strand cDNA. The extension oligonucleotide "TMX24CAnpt" is then added on ice to a final concentration of 0.2 μM. The sequence of "TMX24CAnpt" is 5' GTG CTG GCC GTT GGA AGA GGA GTG CCT GTA CAG GTC CCC GGA

GGC ATC CTC 3' (SEQ ID NO 294) , wherein R is A or G. The three 3' terminal nucleotides are modified to prevent oligo extension. The 2nd strand cDNAs is further elongated off the oligonucleotide by heat denaturing at 94°C for 1 minute, elongating at 68° C for 2 minutes, followed by 4°C. The 2nd strand cDNA is then cleaned up using a QIAGEN spin column (PCR Purification Kit from QIAGEN, Valencia, CA). This step removes the oligonucleotides and allows simple buffer exchange for downstream protocols.

Single primer PCR amplification

PCR amplification of the 2nd strand cDNA is performed using Advantage 2 polymerase mix (Clontech, Palo Alto, CA) and its 10X reaction buffer, dNTPs, and primer "TMX24". The sequence of "TMX24" is 5' GTG CTG GCC GTT GGA AGA GGA GTG 3' (SEQ ID NO 295). The samples is heat denatured at 95°C for 1 minute then cycled 30 times through 95°C for 5 seconds and 68°C for 1 minute. This is followed by an additional 3 minutes at 68°C and a 4°C hold.

Cloning and Sequencing

PCR products of approximately 560 bp are purified using a PCR purification kit (QIAGEN, Valencia, CA), digested by Xho I and BsrG I, gel purified and cloned into a suitable Fab expression vector with the rest of the IgA CH1 constant region.

It will be understood that various modifications may be made to the embodiments described herein. Therefore, the above description should not be construed as limiting, but merely as exemplifications of preferred embodiments. Those skilled in the art will envision other modifications within the scope and spirit of this disclosure.